

Downloaded from <http://ajph.org/> on November 10, 2014

2625	53	3	516	19	AAK72360	Human cytochrome P
2625	99	3	516	17	AAK93167	Human cytochrome P
2625	99	3	516	17	AAW00183	Cytochrome P450IA2
1929.5	73	0	512	16	AAK72365	Human cytochrome P
1929.5	73	0	512	17	AAK93172	Human auxiliary cy
1928.5	72	9	512	16	AAK72366	Human cytochrome P
1928.5	72	9	512	17	AAK93173	Human auxiliary cy
1928.5	72	9	512	17	AAW00185	Human cytochrome P
1927.5	72	9	512	16	AAK72364	Human auxiliary cy
1927.5	72	9	512	17	AAK93171	Human cytochrome P
1910	72	2	512	20	AAK93216	Human cytochrome P

OK
OR

2625	53	3	516	19	AAK72360	Human cytochrome P
2625	99	3	516	17	AAK93167	Human cytochrome P
2625	99	3	516	17	AAW00183	Cytochrome P450IA2
1929.5	73	0	512	16	AAK72365	Human cytochrome P
1929.5	73	0	512	17	AAK93172	Human auxiliary cy
1928.5	72	9	512	16	AAK72366	Human cytochrome P
1928.5	72	9	512	17	AAK93173	Human auxiliary cy
1928.5	72	9	512	17	AAW00185	Human cytochrome P
1927.5	72	9	512	16	AAK72364	Human auxiliary cy
1927.5	72	9	512	17	AAK93171	Human cytochrome P
1910	72	2	512	20	AAK93216	Human cytochrome P

XX Evaluation of safety of a chemical cpd. - using recombinant yeast
 PT expressing human cytochrome p450 and a yeast NADPH-P450 reductase
 XX Examples: Page 18-21; 124pp; English.
 XX The amino acid sequence of the human cytochrome P450 species 1A2. The
 CC 1.5 kb cDNA was amplified by PCR using the primers AAQ87733-4. The
 CC product was cloned into the yeast expression vectors pAAH5N or pARRR to
 CC produce the vectors p1A2 for the expression of the cytochrome P450 alone
 CC or p1A2R co-expressed with the yeast NADPH-P450 reductase, respectively.
 CC The vectors are used in a method for evaluating the safety of a chemical
 CC compound by reacting the chemical compound with recombinantly produced
 CC human cytochrome P450 molecular species 1A2, 2C9 (AAQ87715), 2E1
 CC (AAQ87716) or 3A4 (AAQ87717) or their auxiliary species and variants
 CC (AAQ87718-32) and yeast NADPH-P450 reductase, either as a fused protein
 CC or in cell extracts, and analysing the resulting metabolite to assess the
 CC safety of the chemical compound. The method is useful for determining
 CC whether the chemical compound or its metabolite will be converted into
 CC a carcinogenic or mutagenic form through metabolism in the liver.
 XX Sequence 516 AA;

Query Match 99.3%; Score 2625; DB 16; Length 516;
 Best Local Similarity 97.5%; Pred. No. 1.6e-25;
 Matches 50%; Conservative 1; Mismatches 0; Indels 12; Gaps 1;
 QY 1 MALSSQVPSATALLASAFICLVFWLWKGKLPFPVPRKLSKSHQFQWGLGRLVLTGKN 60
 DB 1 malssqvpsatellasaifclvtwklprprpkulkspgpgwplghvltakn 60
 QY 61 PHALSRMSQRYGDVLOIRIGSTPVLVLSKLDTRQALVRQCDKPKGPDLYTSLTIS 120
 DB 61 phalsrmsqrgydvlgirigstpvvlvlsldtrqalvrqgdkpdkpdytstltidg 120
 QY 121 QSLTFSTDSQVWAAPFRLAQNALNTFASDPASSSSCYLEHVSKEAKALISRLQELM 180
 DB 121 qsltfstdsqvwaarrlraqnalntfasiadpassscylehvskeakalislrlqelm 180
 QY 181 AGPGHEDPYNVVSVANVIGAMCFQHPPESSDEMLSLVKNTHFVETASSGNPLDFPP 240
 DB 181 agpghtfdpnyvsvvanvigamcfrghpessdemslvknthfvetassgnpldfip 240
 QY 241 ILRYLPNALQPKAFNCRFLWFLQKTVOEHYQDFL-----KNSKVCSPRASON 288
 DB 241 ilrylpnalqpkafncrflwflqktvoehyqdf-----knskvsckprason 288
 QY 289 LIPOEKIVNLVNDIFGAGDTVTVAISWSLMVLTKEIOPKIQKELDTVIGRKRPRLS 348
 DB 301 lipqekivnlvndifgagdtvtvaiswslmvltkpeiqkikeldtvigrtrprls 360
 QY 349 DRPQIPYLEAFLETFRHSSTPPTIPHSTRTDTTLNGFTYPRKCCVFWQWVNVIGQEL 408
 DB 361 drpqipyleafletfrhsstlptphsttrtdtllngftypkccvfwqwnvnhdpel 420
 QY 409 WEDSEFRPERFLADGTAINKPLSEKMMFLPGMGKRCICGEVLAKWEIFLFLAILLQGLE 468
 DB 421 wedsefrperfladgtainkplsekmmlfpgmgkrccigevlakweiflailllqgle 480
 QY 469 FSVPPGVKVDLTPYIGLTMKHARCEHVOARLRFSIN 504
 DB 4M1 fsvppgvkvdltptyigltmkharcehvqarlfsin 516
 RESULT 2
 AAR93167
 ID AAR93167 standard; Protein: 516 AA.
 AC AAR93167;
 XX AAR93167;
 DT 11-OCT-1996 (first entry)
 XX

DE Human cytochrome P450 molecular species 1A2 protein.
 XX Human cytochrome P450; amplified; pck; reductase chain reaction; primers
 KW liver; yeast; expression vector; NADPH-P450 reductase; AHH gene; pAAH5N;
 KW evaluation; safety; fusion protein; metabolite; detoxification;
 KW carcinogenic.
 XX Homo sapiens.
 OS JP080506695-A.
 PN 05-MAR-1996.
 PD 15-JUL-1994; 94JP-0164184
 PF 17-JUN-1994; 94JP-0136053.
 PR 20-JUL-1993; 93JP-0201126.
 PR 30-JUL-1993; 93JP-0208279.
 XX (SOMO) SUMITOMO CHEM CO LTD.
 XX WP1: 1996-182311/19.
 DR N-PSDB: AAT28380.
 XX Novel method for the evaluation of the safety of a cpd. - using a
 PT human cytochrome P450 and yeast NADPH reductase to determine whether
 PT the analyte cpd. is detoxified or metabolised to a carcinogen.
 XX Example 1; Page 18-20; 74pp; Japanese.
 CC This is the amino acid sequence of the human cytochrome P450 species
 CC species 1A2 protein. The corresp. 1.5 kb fragment encoding the protein
 CC was amplified from a human liver derived cDNA library using primers
 CC AAT26923-4. The prod. was cloned into the yeast expression vector
 CC pAAH5N to generate plasmid p1A2 for prodn. of the cytochrome only or into
 CC the vector pARRR to generate the plasmid p1A2R for co-prodn. with the
 CC yeast NADPH-P450 reductase. The sequence is placed under control of the
 CC yeast ADH gene promoter and terminator.
 CC The vectors are used in a method for evaluating the safety of a cpd. by
 CC reacting the test cpd. with recombinantly produced human cytochrome P450
 CC mol. species 1A2, 2C9 (2H381), 2E1 (AAT28482), 3A4 (AAT28483) or their
 CC variants (AAT28384-98) together with yeast NADPH-P450 reductase (either
 CC as a fused protein or as a cell extract) and analysing the resultant
 CC metabolite. The cpd. is considered "safe" if it is not detoxified or
 CC rendered carcinogenic or "unsafe" if it is not detoxified or is
 CC metabolised to a carcinogenic cpd.
 CC Sequence 516 AA;

Query Match 99.3%; Score 2625; DB 17; Length 516;
 Best Local Similarity 97.5%; Pred. No. 1.6e-25;
 Matches 50%; Conservative 1; Mismatches 0; Indels 12; Gaps 1;
 QY 1 MALSSQVPSATALLASAFICLVFWLWKGKLPFPVPRKLSKSHQFQWGLGRLVLTGKN 60
 DB 1 malssqvpsatellasaifclvtwklprprpkulkspgpgwplghvltakn 60
 QY 61 PHALSRMSQRYGDVLOIRIGSTPVLVLSKLDTRQALVRQCDKPKGPDLYTSLTIS 120
 DB 61 phalsrmsqrgydvlgirigstpvvlvlsldtrqalvrqgdkpdkpdytstltidg 120
 QY 121 QSLTFSTDSQVWAAPFRLAQNALNTFASDPASSSSCYLEHVSKEAKALISRLQELM 180
 DB 121 qsltfstdsqvwaarrlraqnalntfasiadpassscylehvskeakalislrlqelm 180
 QY 181 AGPGHEDPYNVVSVANVIGAMCFQHPPESSDEMLSLVKNTHFVETASSGNPLDFPP 240
 DB 181 agpghtfdpnyvsvvanvigamcfrghpessdemslvknthfvetassgnpldfip 240
 QY 241 ILRYLPNALQPKAFNCRFLWFLQKTVOEHYQDFL-----KNSKVCSPRASON 288
 DB 241 ilrylpnalqpkafncrflwflqktvoehyqdf-----knskvsckprason 288


```

QY 929 gagaagattgcaacctgtgcaatgacatctttggagcaggatttgacacagtcaccaca 988
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 541 GAGAAGATTGCAACATTTGTAATGACATCTTTGGAGCTGGTTTGAACACTACCA 600
QY 989 gccatctctctgg-agctcatgtacactttgtaccagaacctgagatgacagagaagatcca 1047
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 601 GCCATCACCTGGAGCAATTTGCTAGCTTGTGACATGGGCTAACGTTGACAGCAAGATCCA 660
QY 1048 qaagaagctgacacitgacttggcaggagcggcggccggc-gctctgacagacccc 1106
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 661 TGAGGAGCTGCAACAGCTGGTGGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
QY 1107 agctgacctact-tggagaccttactctggagaccttccgacacctctctcttctggccc 1165
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 721 AGCTGCTAATATGAGAGCTGCTATGCTGAGATGAGATGAGATGAGATGAGATGAGATG 780
QY 1166 ----ttaccatctcccccacagcacacaaggagacacaacgctg-aatggctttcacatccc 1221
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 781 CTTTCAACAATCCCCAAGCAACAGGAGGACACCTCACTAAATGGGTTCCACATGCC 840
QY 1222 caagaaatgctgtgct-ctcgaacacagtgccagtgacacatgacccag-agctgag 1279
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 841 CAAGGAAGCCCTTCTATCTACATACCACTGGCAGGTCCACCATCATGAGGAAGCAGTGG 900
QY 1280 gaggacacctctagttccggcctgagcggtt 1311
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 901 GAAAGACCTTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 932

RESULT 15
BI144965
LOCUS 602904618F1 NCI_GCAP_L19 Mus musculus cDNA linear EST 05-JUL-2001
DEFINITION mRNA sequence.
ACCESSION BI144965
VERSION 1 (bases 1 to 835)
KEYWORDS EST.
SOURCE house mouse
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgaaps-remail.nih.gov
Tissue procurement: Jeffrey E. Green, M.D.
cDNA library preparation: Life Technologies, Inc.
cDNA library arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA sequencing by: Incyte Genomics, Inc.
clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: HAM11138 row: c column: 06
High quality sequence stop: 829
Location/Qualifiers
1..835
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE-5050685"
/clone_lib="NCI_GCAP_L19"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: liver; Vector: pCMV-Sport6; Site:1; NotI;
Site:2; SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_GCAP Library."
BASE COUNT 178 a 255 c 231 g 171 t
ORIGIN

```

```

Query Match 25.6% Score 458.8 DB 10, Length 835;
Best local similarity 78.2% Pred. No. 5, 1e-93;
Matches 640; Conserved 0; Mismatches 167; Indels 11; Gaps 7;
QY 9 acacacccatcccaatctcaagacacccctcctctacagttgacacagatgacatttaccat 68
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 21 ACAACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 78
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 69 ctgtctcctctctcggccacagagcttctctcctcctcctcctcctcctcctcctcctcct 128
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 AAT-----TCTTCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 135
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 129 ggggtctcaggggtttgagcctcgggtcccccagggcctgaaaaggtccacacagacat 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 136 GGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 195
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 189 ggaagcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 248
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 196 GGGGCTTTGGGCTTTGGGCTTTGGGCTTTGGGCTTTGGGCTTTGGGCTTTGGGCTTTGGG 255
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 249 caagagatgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 307
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 256 CACGAGTACATACATACATACATACATACATACATACATACATACATACATACATACAT 315
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 ctgggtcgtgagcctgagacacacacacacacacacacacacacacacacacacacacac 367
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 316 GTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 375
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 aagggcggcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 427
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 376 AAGGCGGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 435
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 agcacagctctctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 487
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 436 AAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 495
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 acctctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 547
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 496 AATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 555
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 548 agcacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 607
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 556 AGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 615
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 608 ttgagcctctacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 667
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 616 TTCTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 675
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 668 ggaacagcactcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 726
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 676 GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 735
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 727 gttcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 784
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 736 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 795
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 785 ctgacctacacctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 822
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 786 TGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 831
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

Search completed: September 8, 2002, 16:54:42
Job time: 7296 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

[illegible]

Run on: September 4, 2002, 17:41:21, record time 33.72 seconds
(with alignment?)
294,466 Million cells updated/sec

Title: US-09-905-370-1
 Project: 2644
 Description: MAI SOSVPESENTI LASSI M'HOGHNY-ADIBESIN 501

Scoring table: Blossum62
Gapop 10.0 , Gapext 0.5

Searched:	56222 seqs, 1729329 residues
total number of hits satisfying chosen parameters:	76222

```
Minimum lds seq length: 0
Maximum lds seq length: 2000000000
```

Post-processing: Minimum Match 98
Maximum Match 100%
Listing first 45 summaries

```
Database :
SPTREMBL_19; *
1: sp_archaea; *
2: sp_bacteria; *
```

```
3: sp_tungt.
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
```

```

7: sp_name;
8: sp_orphanette; *
9: sp_phase; *
10: sp_plant; *

```

```

11: sp_virus; *
12: sp_virus; *
13: sp_vertebrate; *
14: sp_unclassified; *

```

```

15: sp_virus.*
16: sp_bacteria.*
17: sp_archae.*

```

ever, not as one would expect a pretest by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result	Query	Score	Length	DH	ID	Injection
No.	Match					

1	26.25	99.3	516	4	09HX7	09HX7	HOME SH
2	26.2	98.8	516	4	09HX49	09HX49	HOME SH
3	26.5	93.2	516	6	077809	077809	maxima

Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100
1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	

[illegible][illegible]

$\mathbf{1}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}\mathbf{7}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}\mathbf{7}^{\circ}\mathbf{8}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}\mathbf{7}^{\circ}\mathbf{8}^{\circ}\mathbf{9}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}\mathbf{7}^{\circ}\mathbf{8}^{\circ}\mathbf{9}^{\circ}\mathbf{10}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}\mathbf{7}^{\circ}\mathbf{8}^{\circ}\mathbf{9}^{\circ}\mathbf{10}^{\circ}\mathbf{11}^{\circ}$	$\mathbf{1}^{\circ}\mathbf{2}^{\circ}\mathbf{3}^{\circ}\mathbf{4}^{\circ}\mathbf{5}^{\circ}\mathbf{6}^{\circ}\mathbf{7}^{\circ}\mathbf{8}^{\circ}\mathbf{9}^{\circ}\mathbf{10}^{\circ}\mathbf{11}^{\circ}\mathbf{12}^{\circ}$
1	1	1	1	1	1	1	1	1	1
1	2	3	4	5	6	7	8	9	10
1	3	6	10	15	21	28	36	45	55
1	4	10	20	35	56	84	120	165	220
1	5	15	35	70	126	210	330	495	715
1	6	21	56	126	252	462	792	1287	2002
1	7	28	84	210	462	924	1716	3003	4862
1	8	36	120	330	840	1848	3771	7567	13641
1	9	45	165	495	1365	3306	7567	16797	35271
1	10	55	220	715	2002	5278	13641	35271	87531
1	11	66	286	1001	2860	7567	20020	52780	136410
1	12	78	364	1365	3771	10010	28600	75670	200200
1	13	91	462	1848	5278	13641	35271	92400	252250
1	14	105	588	2431	7567	20020	52780	136410	352710
1	15	120	742	3306	10010	28600	75670	200200	527800
1	16	136	936	4374	13641	35271	92400	252250	705435
1	17	153	1170	5852	18480	48620	128700	352710	924000
1	18	171	1456	7929	25225	67200	184800	527800	1364100
1	19	190	1800	10920	35271	92400	252250	705435	2002000
1	20	210	2200	14190	48620	128700	352710	924000	2522500
1	21	231	2660	18009	67200	184800	527800	1364100	3527100
1	22	253	3190	22540	92400	252250	705435	2002000	5278000
1	23	276	3800	28009	128700	352710	924000	2522500	7054350
1	24	300	4500	34650	184800	527800	1364100	3527100	9240000
1	25	325	5300	42780	252250	705435	2002000	5278000	12870000
1	26	351	6200	52780	352710	924000	2522500	7054350	18480000
1	27	378	7210	64770	486200	1287000	3527100	9240000	25225000
1	28	406	8340	78920	672000	1848000	5278000	13641000	35271000
1	29	435	9590	95540	924000	2522500	7054350	20020000	52780000
1	30	465	10980	115800	1287000	3527100	9240000	25225000	70543500
1	31	496	12520	139900	1848000	5278000	13641000	35271000	92400000
1	32	528	14220	168000	2522500				

17	1256	47.5	439	13	Q98S37	Q98S37	1.7	1256	47.5	439	13	Q98S37
18	1115	42.2	335	13	Q98H13	Q98H13	1.9	1115	42.2	335	13	Q98H13
19	1113.5	42.1	339	6	Q98H16	Q98H16	1.9	1113.5	42.1	339	6	Q98H16
20	990	37.4	645	13	Q98H14	Q98H14	2.0	990	37.4	645	13	Q98H14
21	937.5	35.5	646	13	Q98W13	Q98W13	2.1	937.5	35.5	646	13	Q98W13
22	893	33.8	295	13	Q98H39	Q98H39	2.2	893	33.8	295	13	Q98H39
23	769	29.1	183	6	Q98K33	Q98K33	2.3	769	29.1	183	6	Q98K33
24	716	25.3	131	6	Q98W33	Q98W33	2.4	716	25.3	131	6	Q98W33
25	746	23.2	192	10	Q98W42	Q98W42	2.5	746	23.2	192	10	Q98W42
26	746	23.2	192	10	Q98W43	Q98W43	2.6	746	23.2	192	10	Q98W43
27	746	23.2	192	10	Q98W47	Q98W47	2.7	746	23.2	192	10	Q98W47
28	746	23.2	192	10	Q98W41	Q98W41	2.9	746	23.2	192	10	Q98W41
29	744	23.1	195	10	Q98W49	Q98W49	2.9	744	23.1	195	10	Q98W49
30	742	22.1	131	13	Q98W11	Q98W11	3.0	742	22.1	131	13	Q98W11
31	716	27.1	184	10	Q98W40	Q98W40	3.1	716	27.1	184	10	Q98W40
32	711	26.9	184	10	Q98W51	Q98W51	3.2	711	26.9	184	10	Q98W51
33	675	25.5	209	6	Q98K38	Q98K38	3.3	675	25.5	209	6	Q98K38
34	674.5	25.5	618	13	Q98W40	Q98W40	3.4	674.5	25.5	618	13	Q98W40
35	655.5	24.6	611	13	Q98X15	Q98X15	3.5	655.5	24.6	611	13	Q98X15
36	624.5	23.6	501	11	Q98X17	Q98X17	3.6	624.5	23.6	501	11	Q98X17
37	616	23.3	500	11	Q98K73	Q98K73	3.7	616	23.3	500	11	Q98K73
38	615	23.3	500	11	Q98K87	Q98K87	3.8	615	23.3	500	11	Q98K87
39	611.5	23.1	437	13	Q98V10	Q98V10	3.9	611.5	23.1	437	13	Q98V10
40	611	23.1	508	6	Q98W38	Q98W38	4.0	611	23.1	508	6	Q98W38
41	609	23.0	500	6	Q98H33	Q98H33	4.1	609	23.0	500	6	Q98H33
42	599.5	22.7	438	13	Q98A38	Q98A38	4.2	599.5	22.7	438	13	Q98A38
43	599	22.7	534	11	Q98V11	Q98V11	4.3	599	22.7	534	11	Q98V11
44	597	22.6	509	11	Q98V25	Q98V25	4.4	597	22.6	509	11	Q98V25
45	596.5	22.6	509	6	Q98W37	Q98W37	4.5	596.5	22.6	509	6	Q98W37

ACKNOWLEDGMENTS

RESULT

1. **Abstract**
 2. **Introduction**
 3. **Methods**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Tables**
 10. **Figures**
 11. **Supplementary Materials**
 12. **Correspondence**
 13. **Conflict of Interest**
 14. **Acknowledgments**
 15. **References**
 16. **Appendix**
 17. **Tables**
 18. **Figures**
 19. **Supplementary Materials**
 20. **Correspondence**
 21. **Conflict of Interest**
 22. **Acknowledgments**
 23. **References**
 24. **Appendix**
 25. **Tables**
 26. **Figures**
 27. **Supplementary Materials**
 28. **Correspondence**
 29. **Conflict of Interest**
 30. **Acknowledgments**
 31. **References**
 32. **Appendix**
 33. **Tables**
 34. **Figures**
 35. **Supplementary Materials**
 36. **Correspondence**
 37. **Conflict of Interest**
 38. **Acknowledgments**
 39. **References**
 40. **Appendix**
 41. **Tables**
 42. **Figures**
 43. **Supplementary Materials**
 44. **Correspondence**
 45. **Conflict of Interest**
 46. **Acknowledgments**
 47. **References**
 48. **Appendix**
 49. **Tables**
 50. **Figures**
 51. **Supplementary Materials**
 52. **Correspondence**
 53. **Conflict of Interest**
 54. **Acknowledgments**
 55. **References**
 56. **Appendix**
 57. **Tables**
 58. **Figures**
 59. **Supplementary Materials**
 60. **Correspondence**
 61. **Conflict of Interest**
 62. **Acknowledgments**
 63. **References**
 64. **Appendix**
 65. **Tables**
 66. **Figures**
 67. **Supplementary Materials**
 68. **Correspondence**
 69. **Conflict of Interest**
 70. **Acknowledgments**
 71. **References**
 72. **Appendix**
 73. **Tables**
 74. **Figures**
 75. **Supplementary Materials**
 76. **Correspondence**
 77. **Conflict of Interest**
 78. **Acknowledgments**
 79. **References**
 80. **Appendix**
 81. **Tables**
 82. **Figures**
 83. **Supplementary Materials**
 84. **Correspondence**
 85. **Conflict of Interest**
 86. **Acknowledgments**
 87. **References**
 88. **Appendix**
 89. **Tables**
 90. **Figures**
 91. **Supplementary Materials**
 92. **Correspondence**
 93. **Conflict of Interest**
 94. **Acknowledgments**
 95. **References**
 96. **Appendix**
 97. **Tables**
 98. **Figures**
 99. **Supplementary Materials**
 100. **Correspondence**
 101. **Conflict of Interest**
 102. **Acknowledgments**
 103. **References**
 104. **Appendix**
 105. **Tables**
 106. **Figures**
 107. **Supplementary Materials**
 108. **Correspondence**
 109. **Conflict of Interest**
 110. **Acknowledgments**
 111. **References**
 112. **Appendix**
 113. **Tables**
 114. **Figures**
 115. **Supplementary Materials**
 116. **Correspondence**
 117. **Conflict of Interest**
 118. **Acknowledgments**
 119. **References**
 120. **Appendix**
 121. **Tables**
 122. **Figures**
 123. **Supplementary Materials**
 124. **Correspondence**
 125. **Conflict of Interest**
 126. **Acknowledgments**
 127. **References**
 128. **Appendix**
 129. **Tables**
 130. **Figures**
 131. **Supplementary Materials**
 132. **Correspondence**
 133. **Conflict of Interest**
 134. **Acknowledgments**
 135. **References**
 136. **Appendix**
 137. **Tables**
 138. **Figures**
 139. **Supplementary Materials**
 140. **Correspondence**
 141. **Conflict of Interest**
 142. **Acknowledgments**
 143. **References**
 144. **Appendix**
 145. **Tables**
 146. **Figures**
 147. **Supplementary Materials**
 148. **Correspondence**
 149. **Conflict of Interest**
 150. **Acknowledgments**
 151. **References**
 152. **Appendix**
 153. **Tables**
 154. **Figures**
 155. **Supplementary Materials**
 156. **Correspondence**
 157. **Conflict of Interest**
 158. **Acknowledgments**
 159. **References**
 160. **Appendix**
 161. **Tables**
 162. **Figures**
 163. **Supplementary Materials**
 164. **Correspondence**
 165. **Conflict of Interest**
 166. **Acknowledgments**
 167. **References**
 168. **Appendix**
 169. **Tables**
 170. **Figures**
 171. **Supplementary Materials**
 172. **Correspondence**
 173. **Conflict of Interest**
 174. **Acknowledgments**
 175. **References**
 176. **Appendix**
 177. **Tables**
 178. **Figures**
 179. **Supplementary Materials**
 180. **Correspondence**
 181. **Conflict of Interest**
 182. **Acknowledgments**
 183. **References**
 184. **Appendix**
 185. **Tables**
 186. **Figures**
 187. **Supplementary Materials**
 188. **Correspondence**
 189. **Conflict of Interest**
 190. **Acknowledgments**
 191. **References**
 192. **Appendix**
 193. **Tables**
 194. **Figures**
 195. **Supplementary Materials**
 196. **Correspondence**
 197. **Conflict of Interest**
 198. **Acknowledgments**
 199. **References**
 200. **Appendix**
 201. **Tables**
 202. **Figures**
 203. **Supplementary Materials**
 204. **Correspondence**
 205. **Conflict of Interest**
 206. **Acknowledgments**
 207. **References**
 208. **Appendix**
 209. **Tables**
 210. **Figures**
 211. **Supplementary Materials**
 212. **Correspondence**
 213. **Conflict of Interest**
 214. **Acknowledgments**
 215. **References**
 216. **Appendix**
 217. **Tables**
 218. **Figures**
 219. **Supplementary Materials**
 220. **Correspondence**
 221. **Conflict of Interest**
 222. **Acknowledgments**
 223. **References**
 224. **Appendix**
 225. **Tables**
 226. **Figures**
 227. **Supplementary Materials**
 228. **Correspondence**
 229. **Conflict of Interest**
 230. **Acknowledgments**
 231. **References**
 232. **Appendix**
 233. **Tables**
 234. **Figures**
 235. **Supplementary Materials**
 236. **Correspondence**
 237. **Conflict of Interest**
 238. **Acknowledgments**
 239. **References**
 240. **Appendix**
 241. **Tables**
 242. **Figures**
 243. **Supplementary Materials**
 244. **Correspondence**

(a) \mathcal{C}_1 and \mathcal{C}_2 are disjoint

- o Homo Sapiens (human).
- n Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi: Osteichthyes: Actinopterygii: Cyprinodontiformes: Poeciliidae: *Gambusia*.
- o Mammalia: Eutheria: Primates: Carnivora: Canidae: *Canis familiaris*.

$$N^{\frac{1}{2}} \left(\int_0^\infty |f(t)|^2 dt \right)^{\frac{1}{2}}$$
[illegible][illegible]

Section 17.1: Introduction

THE SINGLES ISSUE

July 1947: DSH

Mr. Watt, February 1, 1900

	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2
--	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	---

CO. ROBERT F. A. W. J.

[illegible]

Figure 1 displays 15 small plots showing the distribution of the number of non-zero elements in the vector x for different values of n (from 1 to 15). The x-axis represents the number of non-zero elements (0 to 15), and the y-axis represents the probability. The distributions are unimodal and shift to the right as n increases.

75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100

```

10 71 MSKRFVAVVQIQMPGVVWVIRSFTHQAKTTPQVWVWAGZGQVLSLQIDRKEKALPSS 190
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
12 128 DSHVWAAREELALNAKNEFASLASESSCYTHLHNVKRAKALSKRQGLMAFCHDQ 187
13 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
14 131 DQAVWKTREKLNALPESFTRKSLCYSCVLLHVVKEEYAVKLSNVTFASNSFD 190
15 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
16 188 FAVVSVVANVIGAMTQGHITFSDPEMLSAVKEHHEVVEHANSQFDEETLEETPL 247
17 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
18 191 FHHVSVVANVIGCMFGKRNHDDQELLSVLSDFKQVAGSGNADFTFLRPLPS 250
19 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
20 248 PALGPFKAFNCPFWELKEIVLPHVQVDPSS-----KQDPAVCMPLPQ 293
21 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
22 251 KTFPTFQTHARVTVQVTHVHSPTFNNKEDTFLGLHEDREGLERGVQVSD 310
23 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
24 294 FVHVVATPAGTPTVATLSWLSMVEVTFEPELQSKLQKLLVIGRRPRLSQRL 353
25 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
26 311 KIVGINDLPGAGFGLISALSWAVVLYAVPELQKLRQKMSVGLRPLPLSLKANKL 370
27 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
28 354 PYLEAFITLFRSSSLPFTPHISTRTOTTINQYLPKRCVVFVNGVQVNHDPHWDPS 413
29 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
30 371 PLEAFITLFRSSSLPFTPHICTRTALDQYTPKPEFVPEHQVGNHRTALKKGS 430
31 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
32 413 EEPERPELTADTAIDPQVPEFMHFGMKPSCQGNVAGWHTPLFLAILLQGLHFWP 473
33 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
34 441 SFSPERFNAKGVVWKMFAFVWVMSKPEKSGHATPEPVFLALLVGLRPLPLP 490
35 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
36 474 GVAVDILPIYGLMKHARCHEVQAKLR 500
37 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
38 491 GHPLDLPYGLMKHKRQVLEASLP 516
39 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

```

Query Match 53.2% Score 1405.5 DB 13 Length 519
 Best local similarity 52.0% Pred. No. 134 192
 Matches 268 Conservative 83 Mismatches 141 Indels 15 Gaps 2

```

QY 8 FSAELLASATPCVFWVIELRPEVPEGLKSTPEVWQWPLGLVILKRNHRAER 67
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
12 11 FVSVETLAAVAVVYVLMRELETTEDEGLPKFLLQVQVNVWVWVWVWVWVWVWV 70
13 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
14 11 85APVNAVITPQSTHIVLSKLTQKCAVQVCHIEKPHETSTLTHQSLPSS 127

```

```

10 71 MSKRFVAVVQIQMPGVVWVIRSFTHQAKTTPQVWVWAGZGQVLSLQIDRKEKALPSS 190
11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
12 128 DSHVWAAREELALNAKNEFASLASESSCYTHLHNVKRAKALSKRQGLMAFCHDQ 187
13 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
14 131 DQAVWKTREKLNALPESFTRKSLCYSCVLLHVVKEEYAVKLSNVTFASNSFD 190
15 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
16 188 FAVVSVVANVIGAMTQGHITFSDPEMLSAVKEHHEVVEHANSQFDEETLEETPL 247
17 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
18 191 FHHVSVVANVIGCMFGKRNHDDQELLSVLSDFKQVAGSGNADFTFLRPLPS 250
19 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
20 248 PALGPFKAFNCPFWELKEIVLPHVQVDPSS-----KQDPAVCMPLPQ 293
21 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
22 251 KTFPTFQTHARVTVQVTHVHSPTFNNKEDTFLGLHEDREGLERGVQVSD 310
23 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
24 294 FVHVVATPAGTPTVATLSWLSMVEVTFEPELQSKLQKLLVIGRRPRLSQRL 353
25 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
26 311 KIVGINDLPGAGFGLISALSWAVVLYAVPELQKLRQKMSVGLRPLPLSLKANKL 370
27 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
28 354 PYLEAFITLFRSSSLPFTPHISTRTOTTINQYLPKRCVVFVNGVQVNHDPHWDPS 413
29 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
30 371 PLEAFITLFRSSSLPFTPHICTRTALDQYTPKPEFVPEHQVGNHRTALKKGS 430
31 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
32 413 EEPERPELTADTAIDPQVPEFMHFGMKPSCQGNVAGWHTPLFLAILLQGLHFWP 473
33 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
34 441 SFSPERFNAKGVVWKMFAFVWVMSKPEKSGHATPEPVFLALLVGLRPLPLP 490
35 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
36 474 GVAVDILPIYGLMKHARCHEVQAKLR 500
37 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
38 491 GHPLDLPYGLMKHKRQVLEASLP 516
39 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

```

Query Match 53.2% Score 1405.5 DB 13 Length 519
 Best local similarity 52.0% Pred. No. 134 192
 Matches 268 Conservative 83 Mismatches 141 Indels 15 Gaps 2

```

QY 1 MMLKGVPI CASLHAAVALLGVWVIRKRPVIRKRPVIRKRPVIRKRPVIRKRPVIR 190

```





```

? NAME: Dow, Karen B.
? REGISTRATION NUMBER: 29,684
? REFERENCE PACKET NUMBER: 15080-102-1-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 326-2400
? TELEFAX: (415) 326-2422
? INFORMATION FOR SEQ ID NO. 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 490 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PRT-US95-05744-3

```

```

Query Match 20.8% Score 150; DB 5; Length 490;
Best Local Similarity 29.6%; Pred. No. 150-19;
Matches 145; Conservation 95; Mismatches 204; Indels 16; Gaps 11.

```

```

QY 14 LLASALPOLVFWLKCIGPPVVKGLKSPDIPWVWVCHVITGKNTUWASHEKSY 72
DB 8 VLGLSLLLSLW-----PQSSQTP-KIPPVTPVWVCHVITGKNTUWASHEKSY 61
QY 73 GWLQIPGSTIVIVIPITQIALVQKQPPGPPFQVYNTSLITQVYLTITTSQV 122
DB 13 GWLQIPGSTIVIVIPITQIALVQKQPPGPPFQVYNTSLITQVYLTITTSQV 122
DB 62 GIVTLYVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEK 129
QY 133 WAARRLAGNANFTSIADSPASSSEYLEHIVSEAKLSRQELKACQHPDQV 192
DB 120 WRLRELELTENFQMKES ---LEFVQELAKVLELEKTRASF GUELELL 170
QY 193 VSVAVVIGAMPQCPHPSPSPMLSLVKNRHHVVTASQDHLNIPVLYLPH 247
DB 171 GZANVYVGLTIFHEETFGQELMLKELKELKELKELKELKELKELKELKEL 226
QY 248 PALQRYAYTRHPL-WLQKTVQVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 294
DB 229 TRKELF NVAPRZYVLEFVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEK 242
QY 294 KIVNIVNDELGAGTIVITAKSIVLVIVIFELAPRTQPIIVVLEKIVVLEK 353
DB 286 SLENTAVDLGATTTSTTTPVALLKREVTAVVLEKIVVLEKIVVLEKIVVLEK 342
QY 354 PYLALYLTETPMSSTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 413
DB 346 PYDAVVEVQVYLLPTSLPRAVIGEDIKVNYLIPKGLILLISLVSUNKHTNPE 405
QY 414 PEPPEPTATVATINPISPKMMIPQMKPTPTCTEVLAKVNPITPLDILQQLNP 472
DB 406 MEDPHHLEDEV-NPFSKYPTNTYSQKPTCVGLAKCHLITPLTFLQRLQRL 462
QY 473 INKVDLPLI 482
DB 463 DPKNLDTPEV 472

```

```

RESULT 7
PRT-US95-05744-9
? Sequence 9, Application: EC (muscle) 74;
? GENERAL INFORMATION:
? APPLICANT: GOLDSTEIN, Joyce A.
? APPLICANT: ROMKES-SPARKS, Marjorie
? APPLICANT: DE MURRAY, Scott M.F.
? TITLE OF INVENTION: CLONING, EXPRESSION AND DIAGNOSIS OF HUMAN
? TITLE OF INVENTION: CYTOSOLIC P450 2D19, THE PRINCIPAL JELLSHMENT
? NUMBER OF SEQUENCES: 62
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Townsend and Townsend Kooros and Co.,
? STREET: 379 Lytton Avenue
? CITY: Palo Alto
? STATE: California

```

```

? COUNTRY: US
? ZIP: 94401
? COMPUTER AVAILABLE FROM:
? MEDIA TYPE: floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC 1-5/MS DOS
? SOFTWARE: Patclic Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: PCT/US95/05744
? FILING DATE:
? CLASSIFICATION:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/238,921
? FILING DATE: 06-MAY-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/201,118
? FILING DATE: 22-FEB-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/361,962
? FILING DATE: 09-APR-1992
? ALTERNATE ASSET INFORMATION:
? NAME: Dow, Karen B.
? REGISTRATION NUMBER: 29,684
? REFERENCE PACKET NUMBER: 15080-102-1-1
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (415) 326-2400
? TELEFAX: (415) 326-2422
? INFORMATION FOR SEQ ID NO. 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 490 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? PRT-US95-05744-9

```

```

Query Match 20.8% Score 150; DB 5; Length 490;
Best Local Similarity 29.6%; Pred. No. 150-19;
Matches 145; Conservation 95; Mismatches 204; Indels 16; Gaps 11.
QY 14 LLASALPOLVFWLKCIGPPVVKGLKSPDIPWVWVCHVITGKNTUWASHEKSY 72
DB 8 VLGLSLLLSLW-----PQSSQTP-KIPPVTPVWVCHVITGKNTUWASHEKSY 61
QY 73 GWLQIPGSTIVIVIPITQIALVQKQPPGPPFQVYNTSLITQVYLTITTSQV 122
DB 13 GWLQIPGSTIVIVIPITQIALVQKQPPGPPFQVYNTSLITQVYLTITTSQV 122
DB 62 GIVTLYVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEK 129
QY 133 WAARRLAGNANFTSIADSPASSSEYLEHIVSEAKLSRQELKACQHPDQV 192
DB 120 WRLRELELTENFQMKES ---LEFVQELAKVLELEKTRASF GUELELL 170
QY 193 VSVAVVIGAMPQCPHPSPSPMLSLVKNRHHVVTASQDHLNIPVLYLPH 247
DB 171 GZANVYVGLTIFHEETFGQELMLKELKELKELKELKELKELKELKELKEL 226
QY 248 PALQRYAYTRHPL-WLQKTVQVWVWVWVWVWVWVWVWVWVWVWVWVWVWV 294
DB 229 TRKELF NVAPRZYVLEFVLEKIVVLEKIVVLEKIVVLEKIVVLEKIVVLEK 242
QY 294 KIVNIVNDELGAGTIVITAKSIVLVIVIFELAPRTQPIIVVLEKIVVLEK 353
DB 286 SLENTAVDLGATTTSTTTPVALLKREVTAVVLEKIVVLEKIVVLEKIVVLEK 342
QY 354 PYLALYLTETPMSSTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTTPTT 413
DB 346 PYDAVVEVQVYLLPTSLPRAVIGEDIKVNYLIPKGLILLISLVSUNKHTNPE 405
QY 414 PEPPEPTATVATINPISPKMMIPQMKPTPTCTEVLAKVNPITPLDILQQLNP 472
DB 406 MEDPHHLEDEV-NPFSKYPTNTYSQKPTCVGLAKCHLITPLTFLQRLQRL 462
QY 473 INKVDLPLI 482
DB 463 DPKNLDTPEV 472

```


RESULT 12
PCT-US95-06744 5
Sequence 5, Application 1-7TUS9505744
GENERAL INFORMATION:
APPLICANT: GOLDSIEIN, Joyce A.
APPLICANT: PAPPAS SHAPES, Marjorie
TITLE OF INVENTION: CLIMBER, EXTENSION AND DIAGNOSTIC METHOD
TITLE OF INVENTOR: CYRUSBORE 1453 2019, THE PATENT-LEGAL INFORMATION
TITLE OF INVENTOR: GEORGE MATHURANGIN DETAILER
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Chouteau and Crow
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
RELEASE EXCLUDED: YES, THIS DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
APPLICATION DATA:
APPLICANT NUMBER: 1-7TUS9505744
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 05/097298, 021
FILING DATE: 06 MAY 1994

Query Match 29.7%; Score 546; Hit 2; Length 496;
Best Local Similarity 29.6%; Prod. No. 4,10-49;
Matches 142; conservative 94; mismatches 48; Gaps 11.

[illegible]

Query Match: 20.7%; Score: 546; DB %; Length: 499;
 Read: 100% similarity; 59.6%; Prod. No.: 4,40,49;
 Matched: 14; Coverage: 9%; 10,580,000; 204; 100.0%; 59; 6400; 14



